



# EXHIBIT A

Express Mail Cert. No.: EV 517 995 217 US  
Inventor: Clayton H. Johnson et al.  
Application No.: 10/718,955  
Attorney Docket No.: 55474-294389

>gi|90304992|gb|EAS34623.1| chitin synthase G [Coccidioides immitis RS]  
Length=903

Score = 1593 bits (4126), Expect = 0.0, Method: Composition-based stats.  
Identities = 779/897 (86%), Positives = 827/897 (92%), Gaps = 17/897 (1%)

Query	16	HRLHDL P-SGSQYNLP AEHDASQSLLHQNGPFGPDDPQHHRGGS PVRSPSRYSLTE	74
		HRL D+P +GSQY+LP + DAS+SLL NQGP+ GPFDDP H R SP R SRYSLTE	
Sbjct	17	HRLQDMPPNGSQYHLPQDDASRSL--NQGPYGGPFGDDP--HQRTASPARPASRYSLTE	72
Query	75	SYVTDHPQAQDHY-----GGQMNPAAGFGVPGRVSPYTRSETSSTEAWRQRQAP-GNL	128
		SY TD PQ Y G Q +NPAAGFGVPGRV SPY+RSETSS+AWR+RQAP GNL	
Sbjct	73	SYATD-PQNMSQYNDPMYQQQTDNPAAGFGVPGRVASPYSRSETSSD AWRRRRQAPQGNL	131
Query	129	RRYATR KVKLVQGSVLSVDYPVPSAIQNAVQAKYRNDLEGGSEEFTHMRYTAATCDPNEF	188
		RRYATR KVKLVQGSVLSVDYPVPSAIQNAVQAKYRNDLEGGSEEFTHMRYTAATCDPN+F	
Sbjct	132	RRYATR KVKLVQGSVLSVDYPVPSAIQNAVQAKYRNDLEGGSEEFTHMRYTAATCDPNDF	191
Query	189	TLHNGYNLRPAMYNRHTELLIAITYYNEDKMLTSRTLHGVMQNIRDIVNLKKSEFWNKGK	248
		TLHNGYNLRPAMYNRHTELLIAITYYNEDKMLTSRTLHGVMQNIRDIVN+KKSEFWNKGK	
Sbjct	192	TLHNGYNLRPAMYNRHTELLIAITYYNEDKMLTSRTLHGVMQNIRDIVNKKSEFWNKGK	251
Query	249	PAWQKIVVCLVFDGIDPCDKDLDVLATIGIYQDGVMMKDDVDGKETIAHIFEYTTQLSVT	308
		PAWQKIVV L+FDGIDPCDKD LDVLATIG+YQDGVMMK+DVDGKET+AHIFEYTTQLSVT	
Sbjct	252	PAWQKIVVALIFDGIDPCDKDLDVLATIGVYQDGVMMKRDVDGKETVAHIFEYTTQLSVT	311
Query	309	ANQQLIRPHDDGPSTLPPVQMMFCLKQKNSKKINSHRWLFNAFGRILNPEICILLDAGTK	368
		ANQQLIRPHDDGPSTLPPVQMMFCLKQKNSKKINSHRWLFNAFGRILNPEICILLDAGTK	
Sbjct	312	ANQQLIRPHDDGPSTLPPVQMMFCLKQKNSKKINSHRWLFNAFGRILNPEICILLDAGTK	371
Query	369	PGHKSLLALWEAFYNDKDLGGSCGEIHAMLGKGWKNLINPLVAAQNFEYKISNILDKPLE	428
		PG KSLALWEAFYNDKDLGGSCGEIHAMLGKGW LINPLVAAQNFEYKISNILDKPLE	
Sbjct	372	PGSKSLLALWEAFYNDKDLGGSCGEIHAMLGKGWTKLINPLVAAQNFEYKISNILDKPLE	431
Query	429	SSFYGVSVLPGAFSAYRFRAIMGRPLEQYFHGDHTLSKQLGPKGIEGMNIFKKNMFLAED	488
		SSFYGVSVLPGAFSAYRFRAIMGRPLEQYFHGDHTLSKQLGPKGIEGMNIFKKNMFLAED	
Sbjct	432	SSFYGVSVLPGAFSAYRFRAIMGRPLEQYFHGDHTLSKQLGPKGIEGMNIFKKNMFLAED	491
Query	489	RILCFELVAKAGSKWHL SYVSKSGETDVPEGAPEFIGQRRRWLNGSFAASIYSLMHFGR	548
		RILCFELVAKAGSKWHL+YVK+SKGETDVPEGAPEFI QRRRWLNGSFAASIY+LMHFGR	
Sbjct	492	RILCFELVAKAGSKWHLTYVKASKGETDVPEGAPEFISQRRRWLNGSFAASIYALMHFGR	551
Query	549	MYKSGHNLLRMFFFHIIQMIYNTCTVIMTW FALASYWLTTSVIMDLVGNPPAPESGSTQRA	608
		MYKSGHN+LRMFFFHIIQ+YNT TV +TW FALA+YWLTTSVIMDLVGNP + QRA	
Sbjct	552	MYKSGHNILRMFFFHIIQMLYNTFTVFLTW FALAA YWLTTSVIMDLVGNP---NQEQQRA	607
Query	609	FPPGNTATPIVNTVlkylaflllqfilalGNRPKGSKHSYITSFVVFGLIQLYIIVLS	668
		FPPGN TPI+NTVLKYLYL FLLLQFILALGNRPKGSKHSYITSF++FG++QLYI++LS	
Sbjct	608	FPPGNKVTPI LNTVLKYLYLG FLLLQFILALGNRPKGSKHSYITSFILGLVQLYIIVLS	667
Query	669	MYLVVRAFSGGTLAFTTDKGIGEF LKSFFSSESGPIIIIALAATFGLYFVASFMYLDPWH	728
		MYLVVRAFS G++ F TDKG+ FLKSFF S+ GII+IALAATFGLYFVASFMY+DPWH	
Sbjct	668	MYLVVRAFS-GSVDFETDKGVDGFLKSFFSGSDSAGIIVIALAATFGLYFVASFMYMDPWH	726
Query	729	MFTSFPA YLLIMSSYINILMVYAFSNWHDVSWGTGKADKADALPSAQTQKEDDGKAAVIE	788
		MFTSFPA YLLIMSSYINILMVYAFSNWHDVSWGTGK+DKADALPSAQT KED GKAAVIE	
Sbjct	727	MFTSFPA YLLIMSSYINILMVYAFSNWHDVSWGTGKSDKADALPSAQTTKEDDGKAAVIE	786
Query	789	EIDKPQADIDSQFESTVKRALTPYVEPKVKEGKSLDDSYKSFRTLVTLWLFNSGILAVA	848
		EIDKPQADIDSQFE+TVKRALTP+VEPKV E KSL+DSYKSFRTLV W+FSN +LAV	

Sbjct 787 EIDKPQADIDSQFEATVKRALTPFVEPKVDEKKSLEDSYKSFRTRLVASWIFSNALLAVL 846

Query 849 ITSEDVNKGFTSRATSRTHFFHALLWATAALSLIRFTGACWFLGRTGIMCCFARR 905  
ITS+ VNK GFTS+AT RT +FF ALLWATAALSLIRF GACWFLG++GIMCCFARR

Sbjct 847 ITSDSVNKLGFTSQATDRTANFFRALLWATAALSLIRFIGACWFLGKSGIMCCFARR 903